GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 16, 2005, 15:48:46 ; Search time 177 Seconds
(without alignments)
454.217 Million cell updates/sec

Title: US-10-730-034-1
Perfect score: 812
Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKEDELGDRSIMFTVQNED 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	811	99.9	189	2	Q6WWJ7	Q6wwj7 homo sapien
2	811	99.9	193	1	IL18_HUMAN	Q14116 homo sapien
3	798	98.3	193	2	Q96KJ8	Q96kj8 homo sapien
4	792	97.5	193	2	Q9BGI5	Q9bgi5 macaca mula
5	659	81.2	193	1	IL18_HORSE	Q9xsq7 equus cabal
6	659	81.2	193	2	Q6T573	Q6t573 bubalus bub
7	659	81.2	193	2	Q6TLW4	Q6tlw4 bubalus bub
8	654	80.5	178	2	Q9MZL8	Q9mzl8 bos taurus
9	654	80.5	193	1	IL18_BOVIN	Q9tu73 bos taurus
10	648	79.8	193	2	Q9GL09	Q9gl09 ovis aries
11	647	79.7	159	2	Q6QVC4	Q6qvc4 capra hircu
12	637	78.4	192	1	IL18_PIG	O19073 sus scrofa
13	634	78.1	192	2	Q95M33	Q95m33 felis silve
14	633	78.0	192	2	Q865B8	Q865b8 felis silve
15	626	77.1	192	2	Q9N1P7	Q9n1p7 sus scrofa
16	613	75.5	193	1	IL18_CANFA	Q9xsr0 canis famil
17	578	71.2	177	2	Q6STL7	Q6stl7 sus scrofa
18	536.5	66.1	195	2	Q80Y07	Q80y07 meriones un
19	515	63.4	189	2	Q80SS8	Q80ss8 mus musculu
20	515	63.4	192	1	IL18_MOUSE	P70380 mus musculu
21	514.5	63.4	194	1	IL18_RAT	P97636 rattus norv
22	501	61.7	192	2	Q6USQ6	Q6usq6 mus musculu
23	441	54.3	196	2	Q91Z66	Q91z66 sigmodon hi
24	313	38.5	84	2	Q95LE7	Q95le7 canis famil
25	204	25.1	45	2	Q9NQ49	Q9nq49 homo sapien
26	193	23.8	211	2	Q98SQ1	Q98sq1 anas platyr
27	184.5	22.7	198	2	Q8AV26	Q8av26 meleagris g
28	182.5	22.5	169	2	Q6IT44	Q6it44 gallus gall
29	182.5	22.5	198	2	Q9I8D2	Q9i8d2 gallus gall
30	178.5	22.0	196	1	IL18_CHICK	Q8qfq8 gallus gall
31	116	14.3	199	2	Q70PK1	Q70pk1 oncorhynchu
32	111	13.7	182	2	Q6EV48	Q6ev48 oncorhynchu
33	111	13.7	199	2	Q6EV49	Q6ev49 oncorhynchu
34	88	10.8	181	2	Q6F0J1	Q6f0j1 mesoplasma
35	88	10.8	4705	1	FAT2_DROME	Q9vw71 drosophila
36	86.5	10.7	376	2	Q8K4E6	Q8k4e6 mus musculu
37	86.5	10.7	376	2	Q8K4E7	Q8k4e7 mus musculu
38	85.5	10.5	867	2	Q7RNN8	Q7rnn8 plasmodium
39	85	10.5	252	2	Q8JZN4	Q8jzn4 mus musculu
40	84.5	10.4	376	2	Q8K4E8	Q8k4e8 mus musculu
41	84	10.3	1101	2	Q6CIC3	Q6cic3 kluyveromyc
42	83.5	10.3	182	2	O43031	O43031 schizosacch
43	83.5	10.3	454	2	Q8HZU5	Q8hzu5 tonatia sau
44	83.5	10.3	454	2	Q8HZU6	Q8hzu6 tonatia sau
45	83.5	10.3	454	2	Q8HZU7	Q8hzu7 tonatia sau

ALIGNMENTS

RESULT 1
Q6WWJ7
ID Q6WWJ7 PRELIMINARY; PRT; 189 AA.
AC Q6WWJ7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE DELTA3PRO-IL-18.
GN Name=IL18;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gaggero A., De Ambrosis A., Mezzanzanica D., Piazza T., Rubartelli A.,
RA Figini M., Canevari S., Ferrini S.;
RT "A novel isoform of pro-interleukin-18 expressed in ovarian tumors is
RT resistant to caspase-1 and -4 processing.";
RL Oncogene 0:0-0(2004).
DR EMBL; AY266351; AAP92112.1; -.
DR InterPro; IPR008996; Cytok_IL1_like.
SQ SEQUENCE 189 AA; 21896 MW; A8BA275CF713A4B6 CRC64;

Query Match 99.9%; Score 811; DB 2; Length 189;
Best Local Similarity 99.4%; Pred. No. 1.5e-67;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 92

Qy         61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 152

Qy        121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
              |||||||||||||||||||||||||||||||||||||
Db        153 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 189
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RESULT 2
IL18_HUMAN
ID IL18_HUMAN STANDARD; PRT; 193 AA.
AC Q14116; O75599;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN Name=IL18; Synonyms=IGIF;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=96247646; PubMed=8666798;
RA   Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,
RA   Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,
RA   Fukuda S., Ikeda M., Okamura H., Kurimoto M.;
RT   "Cloning of the cDNA for human IFN-gamma-inducing factor, expression
RT   in Escherichia coli, and studies on the biologic activities of the
RT   protein.";
RL   J. Immunol. 156:4274-4279(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Yong D., Guixin D., Lihua H., Haitao W.;
RT   "Cloning and sequencing of the cDNA for precursor hIL-18.";
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Liu J., Peng X., Yuan J., Qiang B.;
RT   "Cloning of human interleukin 18 cDNA.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Urinary bladder;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   SEQUENCE OF 2-193 FROM N.A.
RC   TISSUE=Peripheral blood;
RA   Conti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;
RL   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Augments natural killer cell activity in spleen cells
CC       and stimulates interferon gamma production in T helper type I
CC       cells.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the IL-1 family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D49950; BAA08706.1; -.
DR   EMBL; AF077611; AAC27787.1; -.
DR   EMBL; AY044641; AAK95950.1; -.
DR   EMBL; BC007007; AAH07007.1; -.
DR   EMBL; BC007461; AAH07461.1; -.
DR   EMBL; U90434; AAB50010.1; -.
DR   PDB; 1J0S; NMR; A=37-193.
DR   OGP; Q14116; -.
DR   Genew; HGNC:5986; IL18.
DR   H-InvDB; HIX0010123; -.
DR   MIM; 600953; -.
DR   GO; GO:0005576; C:extracellular; TAS.
DR   GO; GO:0005125; F:cytokine activity; TAS.
DR   GO; GO:0004871; F:signal transducer activity; TAS.
DR   GO; GO:0001525; P:angiogenesis; IDA.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0042033; P:chemokine biosynthesis; TAS.
DR   GO; GO:0042253; P:granulocyte macrophage colony-stimulating f. . .; TAS.
DR   GO; GO:0006955; P:immune response; TAS.
DR   GO; GO:0008625; P:induction of apoptosis via death domain rec. . .; ISS.
DR   GO; GO:0042095; P:interferon-gamma biosynthesis; TAS.
DR   GO; GO:0042231; P:interleukin-13 biosynthesis; TAS.
DR   GO; GO:0042094; P:interleukin-2 biosynthesis; TAS.
DR   GO; GO:0042104; P:positive regulation of activated T-cell pro. . .; IDA.
DR   GO; GO:0030155; P:regulation of cell adhesion; IDA.
DR   GO; GO:0030431; P:sleep; ISS.
DR   GO; GO:0042092; P:T-helper 2 type immune response; TAS.
DR   InterPro; IPR008996; Cytok_IL1_like.
DR   InterPro; IPR000975; Interleukin_1.
DR   SMART; SM00125; IL1; 1.
KW   3D-structure; Cytokine.
FT   PROPEP        1     36       By similarity.
FT   CHAIN        37    193       Interleukin-18.
FT   CONFLICT     66     66       F -> L (in Ref. 2).
FT   CONFLICT     86     86       S -> R (in Ref. 2).
FT   CONFLICT    191    191       N -> S (in Ref. 2).
SQ   SEQUENCE   193 AA;  22326 MW;  323C62C203788D55 CRC64;

  Query Match             99.9%;  Score 811;  DB 1;  Length 193;
  Best Local Similarity   99.4%;  Pred. No. 1.6e-67;
  Matches  156;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 96

Qy         61 AVTISVKCEKISXLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 120
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         97 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSY 156

Qy        121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 157
              |||||||||||||||||||||||||||||||||||||
Db        157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED 193


RESULT 3
Q96KJ8
ID   Q96KJ8      PRELIMINARY;      PRT;   193 AA.
AC   Q96KJ8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Interleukin 18.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ying P., Jianxin L.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF380360; AAK57024.1; -.
DR   HSSP; Q14116; 1J0S.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR008996; Cytok_IL1_like.
DR   InterPro; IPR000975; Interleukin_1.
DR   SMART; SM00125; IL1; 1.
SQ   SEQUENCE   193 AA;  22323 MW;  2E500205D1B7E5F7 CRC64;
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